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```
                                                                    50
                1
mCD40Alt19      MVSLPRLCAL WGCLLTAVHL GQCVTCSDKQ YLHDGQCCDL CQPGSRLTSH
mCD40Alt8       MVSLPRLCAL WGCLLTAVHL GQCVTCSDKQ YLHDGQCCDL CQPGSRLTSH
mCD40Alt6Corected MVSLPRLCAL WGCLLTAVHL GQCVTCSDKQ YLHDGQCCDL CQPGSRLTSH
mCD40-wt        MVSLPRLCAL WGCLLTAVHL GQCVTCSDKQ YLHDGQCCDL CQPGSRLTSH
mcd40-pFB1-1-5  MVSLPRLCAL WGCLLTAVHL GQCVTCSDKQ YLHDGQCCDL CQPGSRLTSH

                                                                   100
               51
mCD40Alt19      CTALEKTQCH PCDSGEFSAQ WNREIRCHQH RHCEP..... ...NQGLRVK
mCD40Alt8       CTALEKTQCH PCDSGEFSAQ WNREIRCHQH RHCEP..... ...NQGLRVK
mCD40Alt6Corected CTALEKTQCH PCDSGEFSAQ WNREIRCHQH RHCEPSAWGC LGRDQGLRVK
mCD40-wt        CTALEKTQCH PCDSGEFSAQ WNREIRCHQH RHCEP..... ...NQGLRVK
mcd40-pFB1-1-5  CTALEKTQCH PCDSGEFSAQ WNREIRCHQH RHCEP..... ...NQGLRVK

                                                                   150
               101
mCD40Alt19      KEGTAESDTV CTCKEGQHCT SKDCEACAQH TPCIPGFGVM EMATE.TTDT
mCD40Alt8       KEGTAESDTV CTCKEGQHCT SKDCEACAQH TPCIPGFGVM EMATE.TTDT
mCD40Alt6Corected KEGTAESDTV CTCKEGQHCT SKDCEACAQH TPCIPGFGVM EMATE.TTDT
mCD40-wt        KEGTAESDTV CTCKEGQHCT SKDCEACAQH TPCIPGFGVM EMATE.TTDT
mcd40-pFB1-1-5  KEGTAESDTV CTCKEGQHCT SKDCEACAQH TPCIPGFGVM EMAVRIRTWR
```

Fig. 1

```
                 151                                                      200
      mCD40Alt19 VCHPCPVGFF SNQSSLFEKC YPWTRFKVPD ASPAGHSCRD GHPHHRFRGV
       mCD40Alt8 VCHPCPVGFF SNQSSLFEKC YPWTRFKVPD ASPAGHSCRD GHPHHHFRGV
mCD40Alt6Corected VCHPCPVGFF SNQSSLFEKC YPWTRFKVPD ASPAGHSCRD GHPHHHFRGV
       mCD40-wt  VCHPCPVGFF SNQSSLFEKC YPWTSCEDKN LEVLQKGTSQ TNVICGLKSR
   mcd40-pFB1-1-5 SYRKERVRLM SSVV~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

                 201                                                      250
      mCD40Alt19 SLYQ~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       mCD40Alt8 SLYQKGGQET KG~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
mCD40Alt6Corected SLYQKGGQET KG~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       mCD40-wt  MRALLVIPVV MGILITIFGV FLYIKKVVKK PKDNEMLPPA ARRQDPQEME
   mcd40-pFB1-1-5 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

                 251                                                    298
      mCD40Alt19 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~
       mCD40Alt8 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~
mCD40Alt6Corected ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~
       mCD40-wt  DYPGHNTAAP VQETLHGCQP VTQEDGKESR ISVQERQVTD SIALRPLV
   mcd40-pFB1-1-5 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~
```

Fig. 1(Cont.)

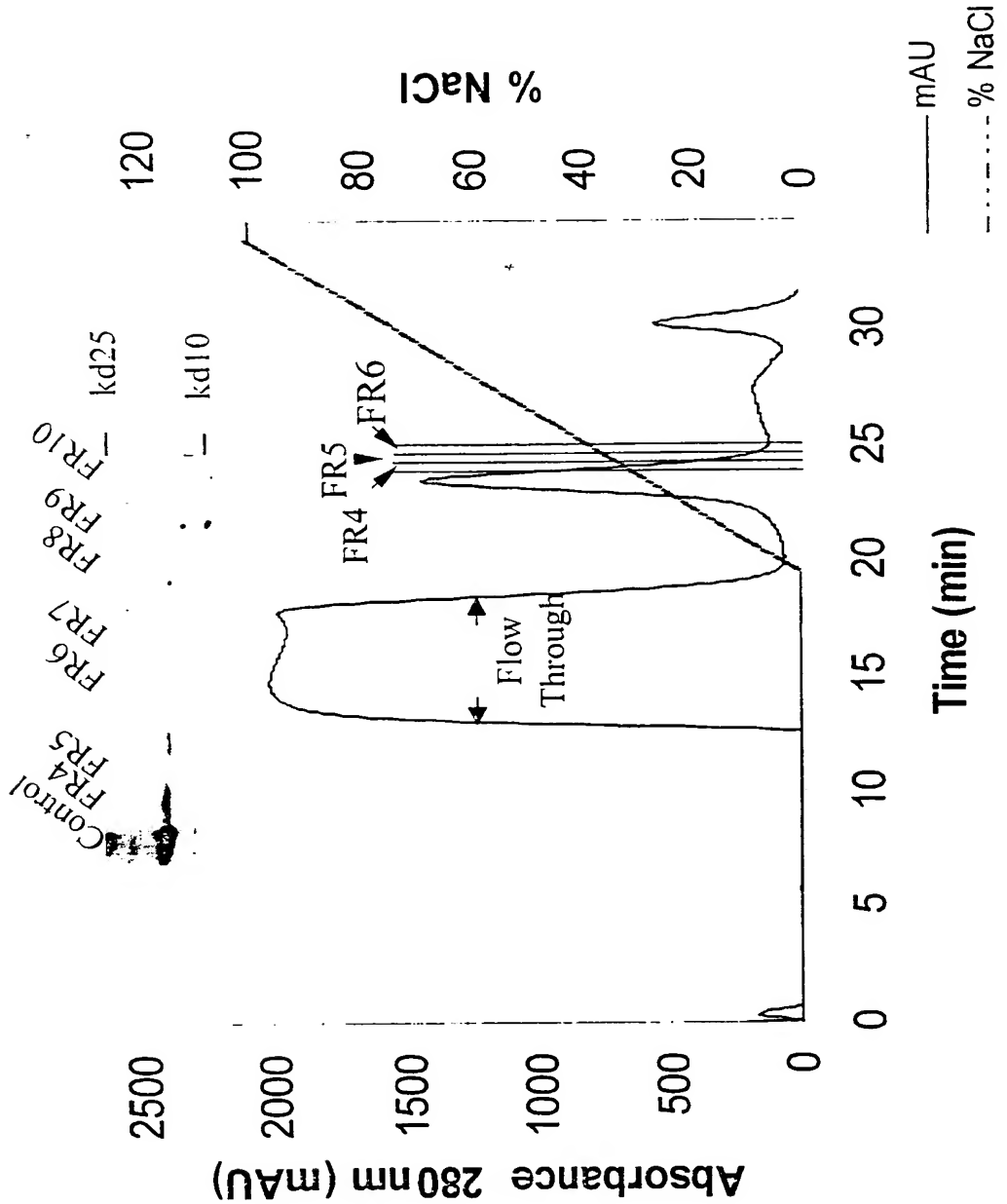
Absorbance 280nm (mAU)
2500
2000
1500
1000
500
0
% NaCl
120
100
80
60
40
20
0
Time (min)
0
5
10
15
20
25
30
mAU
% NaCl
Flow Through
FR4
FR5
FR6
Control
FR4
FR5
FR6
FR7
FR8
FR9
FR10
kd10
kd25

FIG.2

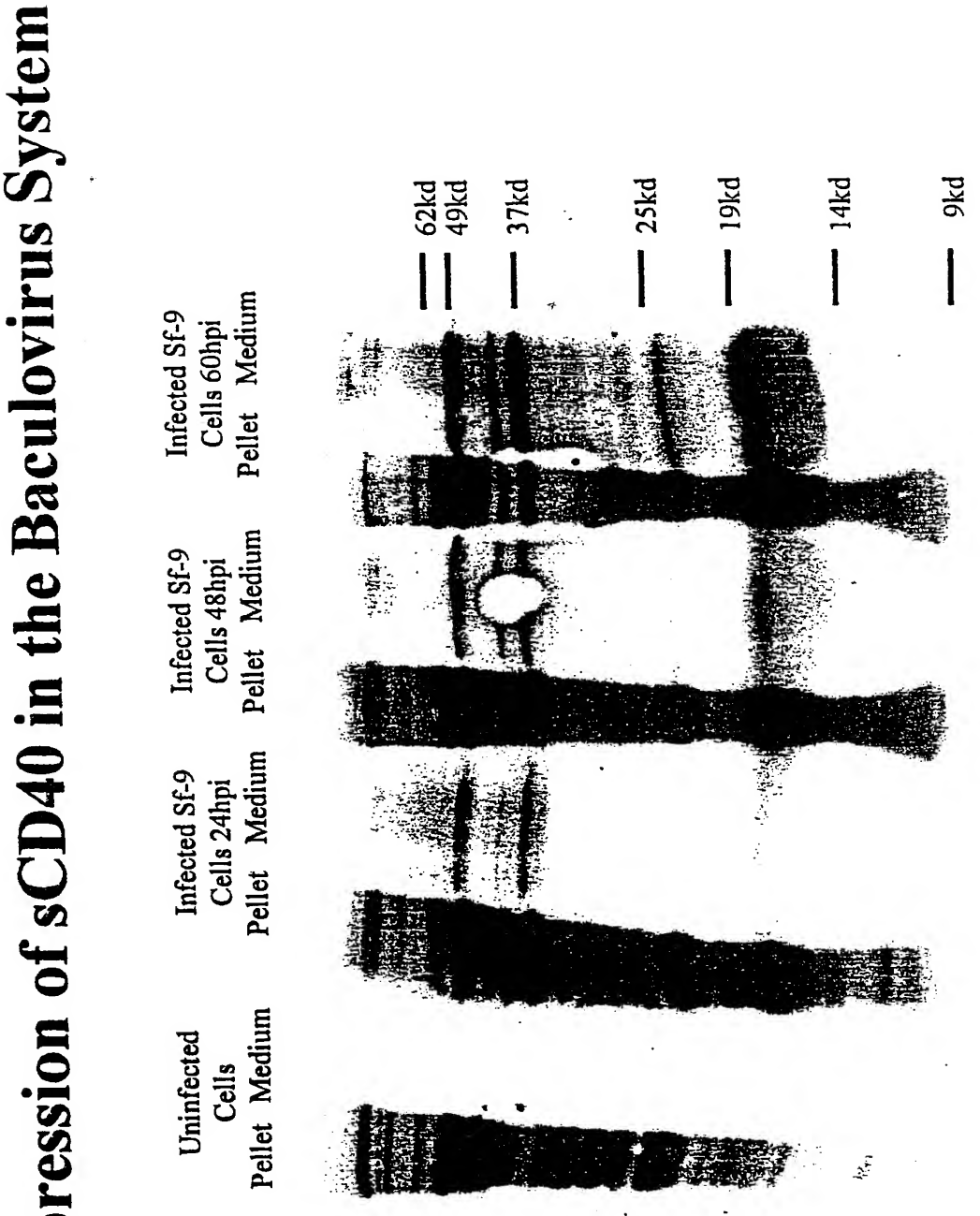
Expression of sCD40 in the Baculovirus System
Uninfected Cells Pellet
Medium
Infected Sf-9 Cells 24hpi Pellet
Medium
Infected Sf-9 Cells 48hpi Pellet
Medium
Infected Sf-9 Cells 60hpi Pellet
Medium
62kd
49kd
37kd
25kd
19kd
14kd
9kd

Fig. 3

```
1   ..............................ATG 3
                                   |||
1   gcctcgctcgggcgcccagtggtcctgccgcctggtctcacctcgccatg 5

4   GTTCGTCTGCCTCTGCAGTGCGTCCTCTGGGGCTGCTTGCTGACCGCTGT 53
    |||||||||||||||||||||||||||||||||||||||||||||||||
51  gttcgtctcctctgcagtgcgtcctctggggctgcttgctgaccgctgt 100

54  CCATCCAGAACCACCCACTGCATGCAGAGAAAAACAGTACCTAATAAACA 103
    |||||||||||||||||||||||||||||||||||||||||||||||||
101 ccatccagaaccacccactgcatgcagagaaaaacagtacctaataaaca 150

104 GTCAGTGCTGTTCTTTGTGCCAGCCAGGACAGAAACTGGTGAGTGACTGC 153
    |||||||||||||||||||||||||||||||||||||||||||||||||
151 gtcagtgctgttctttgtgccaggacagaaactggtgagtgactgc 200

154 ACAGAGTTCACTGAAACGGAATGCCTTCCTTGCGGTGAAAGCGAATTCCT 203
    |||||||||||||||||||||||||||||||||||||||||||||||||
201 acagagttcactgaaacggaatgccttcctttgcggtgaaagcgaattcct 250

204 AGACACCTGGAACAGAGAGACACACTGCCACCAGCACAAATACTGCGACC 253
    |||||||||||||||||||||||||||||||||||||||||||||||||
251 agacacctggaacagagagacacactgccaccagcacaaatactgcgacc 300
```

Fig.4


254 CCAACCTAGGGCTTCGGGTCCAGCAGAAGGGCACCTCAGAAACAGACACC 303
301 ccaacctagggcttcgggtccagcagaagggcacctcagaaacagacacc 350
304 ATCTGCACCTGTGAAGAAGGCTGGCACTGTACGAGTGAGGCCTGTGAGAG 353
351 atctgcacctgtgaagaaggctggcactgtacgagtgaggcctgtgagag 400
354 CTGTGTCCTGCACCGCTCATGCTCGCCCGGCTTTGGGGTCAAGCAGATT. 402
401 ctgtgtcctgcaccgctcatgctcgcccggctttggggtcaagcagattg 450
403 .....GCTGTGA 409
501 tccaatgtgtcatctgctttcgaaaaatgtcacccttggacaagctgtga 550
410 GACCAAAGACCTGGTTGTGCAACAGGCAGGCACAAACAAGACTGATGTTG 459
551 gaccaaagacctggttgtgcaacaggcaggcacaaacaagactgatgttg 600
460 TCTGTGGTCCCCAGGATCGGCTGAGAGCCCTGGTGGtGATCCCCATCATC 509
601 tctgtggtccccaggatcggctgagagccctggtggtgatccccatcatc 650

Fig.4(Cont.)

```
510 TTCGGGATCCTGTTTGC..................................... 526
    |||||||||||||||||
651 ttcgggatcctgtttgccatccctcttggtgctggtctttatcaaaaaggt 700
```

Fig.4(Cont.)

```
64  CCCGGGATGGTTCGTCTGCCTCTGCAGTGCGTCCTCTGGGGCTGCTTGCT 113
    |  ||  |||||||||||||||||||||||||||||||||||||||||||
42  ctcgccatggttcgtctgcctctgcagtgcgtcctctggggctgcttgct  91

114 GACCGCTGTCCATCCAGAACCACCCACTGCATGCAGAGAAAAACAGtACC 163
    ||||||||||||||||||||||||||||||||||||||||||||||||||
92  gaccgctgtccatccagaaccacccactgcatgcagagaaaaacagtacc 141

164 TAATAAACAGTCAGTGCTGTTCTTTGTGCCAGCCAGGACAGAAACTGGTG 213
    ||||||||||||||||||||||||||||||||||||||||||||||||||
142 taataaacagtcagtgctgttctttgtgccagccaggacagaaaactggtg 191

214 AGTGACTGCACAGAGTTCACTGAAACGGAATGCCTTCCTTGCGGTGAAAG 263
    ||||||||||||||||||||||||||||||||||||||||||||||||||
192 agtgactgcacagagttcactgaaacggaatgccttccttgcggtgaaag 241

264 CGAATTCCTAGACACCTGGAACAGAGAGACACACTGCCACCAGCACAAAT 313
    ||||||||||||||||||||||||||||||||||||||||||||||||||
242 cgaattcctagacacctggaacagagagacacactgccaccagcacaaat 291
```

Fig. 5

```
314 ACTGCGACCCCAACCTAGGGCTTCGGGTCCAGCAGAAGGGCACCTCAgAA 363
    |||||||||||||||||||||||||||||||||||||||||||||||||||
292 actgcgaccccaacctagggcttcgggtccagcagaagggcacctcagaa 341

364 ACAGACACCATCTGCACCTGTGAAGAGGCTGGCACTGTACGAGTGAGGC 413
    |||||||||||||||||||||||||||||||||||||||||||||||||
342 acagacaccatctgcacctgtgaagaaggctggcactgtacgagtgaggc 391

414 CTGTGAGAGCTGTGTCCTGCACCGCTCATGCTCGCCCGGcTTTGGGGTCA 463
    |||||||||||||||||||||||||||||||||||||||||||||||||
392 ctgtgagagctgtgtcctgcaccgctcatgctcgcccggctttgggGtca 441

464 AGCAGATTGCT..........................................  474
    |||||||||||
442 agcagattgctacaggggtttctgataccatctgcgagccctgcccagtc 491

475 ....TGTGAGACCAAAGACCTGGTTGTGCAACAGGCAGGCACACAAACAAGA 520
    ||||||||||||||||||||||||||||||||||||||||||||||||||
542 aagctgtgagaccaaagacctggttgtgcaacaggcaggcacacaaacaaga 591

521 CTGATGTTGTCTGTGGTCCCCAAGATCGGCTGAGAGCCCTGGTGGTGATC 570
    ||||||||||||||||||||||||||||||||||||||||||||||||||
592 ctgatgttgtctgtggtccccaggatcggctgagagccctggtggtgatc 641
```

Fig. 5 (Cont.[1])

```
571 CCCATCATCTTCGGGATCCTGTTTGCCATCCTCTTGGTGCTGGTCTTTAT 620
    ||||||||||||||||||||||||||||||||||||||||||||||||||
642 cccatcatcttcgggatccctgtttgccatcctctttggtgctggtctttat 691

621 CAAAAGGTGGCCAAGAAGCCAACCAATAAGGCCCCCCCACCCCAAGCAGG 670
    ||||||||||||||||||||||||||||||||||||||||||||||||||
692 caaaaaggtggccaagaagccaaccaataaggcccccccacccccaagcagg 741

671 AACCCCAGGAGATCAATTTTCCCGACGATCTTCCTGGCTCCAACACTGCT 720
    ||||||||||||||||||||||||||||||||||||||||||||||||||
742 aaccccaggagatcaattttccccgacgatctttcctggctcccaacactgct 791

721 GCTCCAGTGCAGGAGACTTTACATGGATGCCAACCGGTCACCCAGGAGGA 770
    ||||||||||||||||||||||||||||||||||||||||||||||||||
792 gctccagtgcaggagactttacatggatgccaaccggtcacccaggagga 841

771 TGGCAAGAGAGTCGCATCTCAGTGCAGGAGACAGTGAGGCTGCACCC 820
    ||||||||||||||||||||||||||||||||||||||||||||||||||
842 tggcaaagagagtcgcatctcagtgcaggagacagtgaggctgcaccc 891
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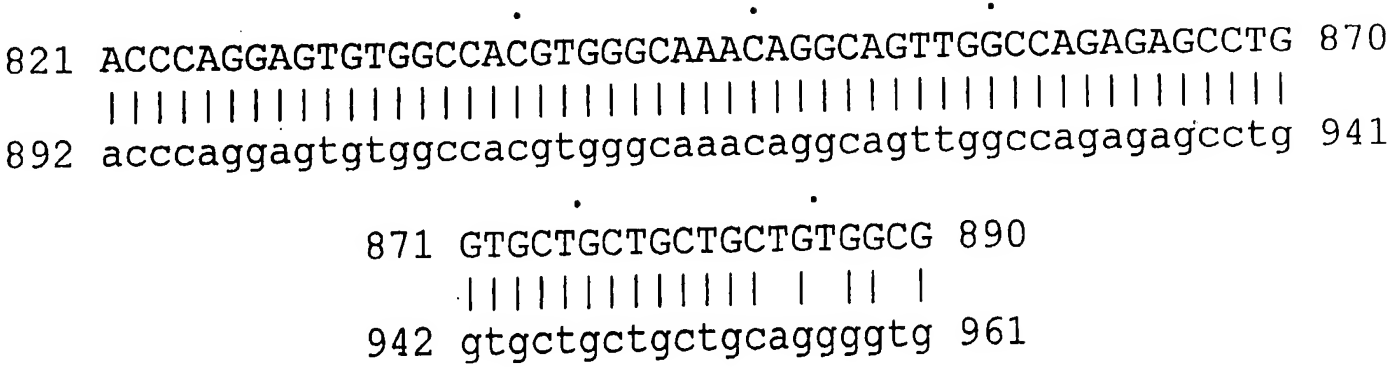
Fig. 5 (Cont.[2])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892 acccaggagtgtggccacgtgggcaaacaggcagttggccagagagcctg 941
871 GTGCTGCTGCTGCTGTGGCG 890
942 gtgctgctgctgcaggggtg 961

Fig. 5 (Cont.[3])

```
  1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSD  50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSD  50

 51 CTEFTETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETD 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 CTEFTETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETD 100

101 TICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTIC 143
    |||||||||||||||||||||||||||||||||||||||||||
101 TICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIAVRPKTWLC 143
```

Fig. 6